

Fig. 1

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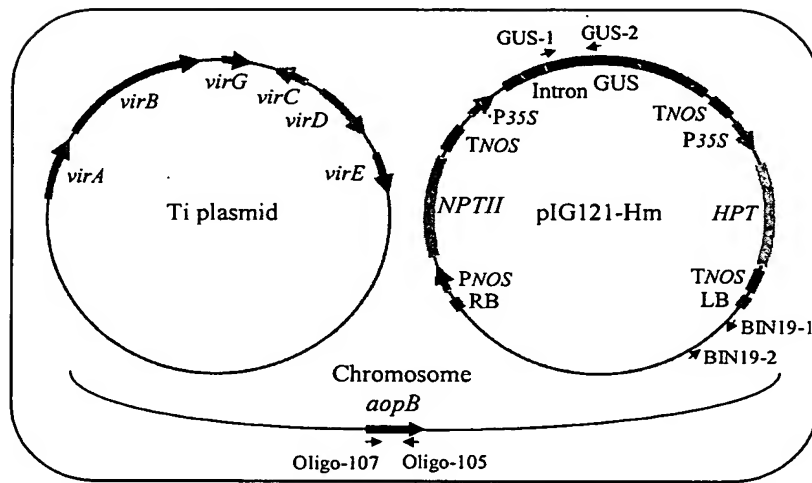


Fig. 2

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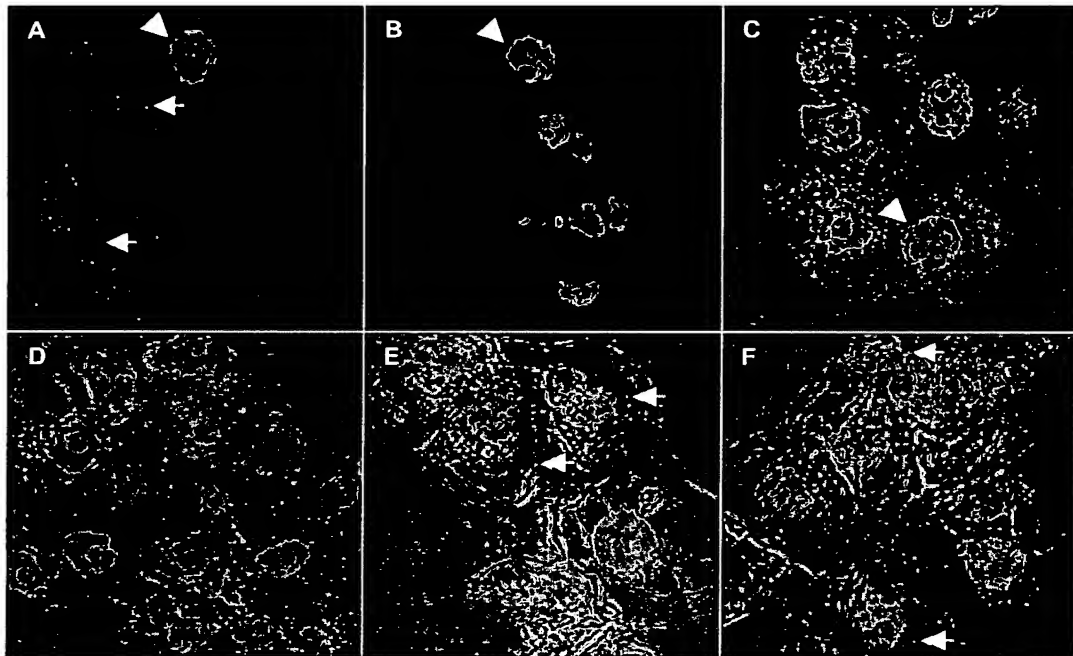


Fig. 3

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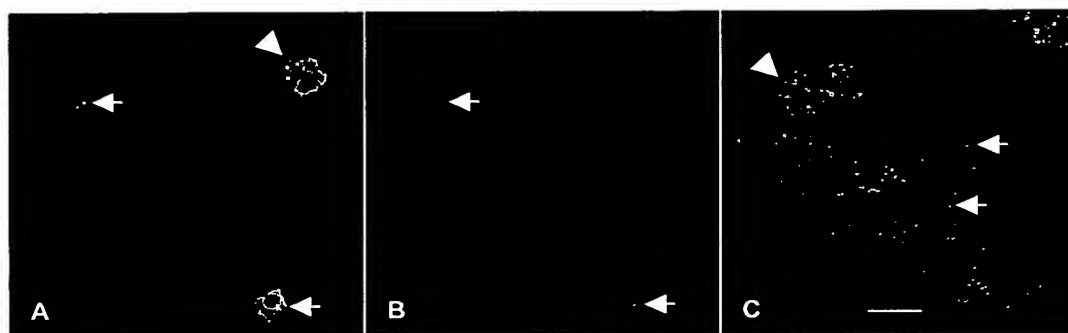


Fig. 4

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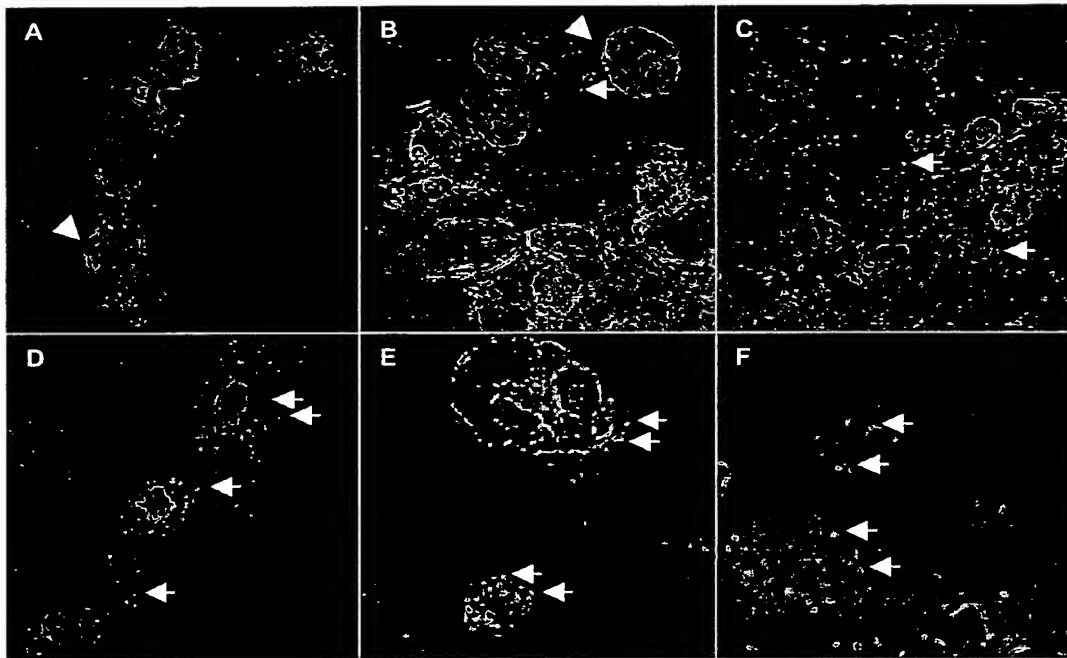


Fig. 5

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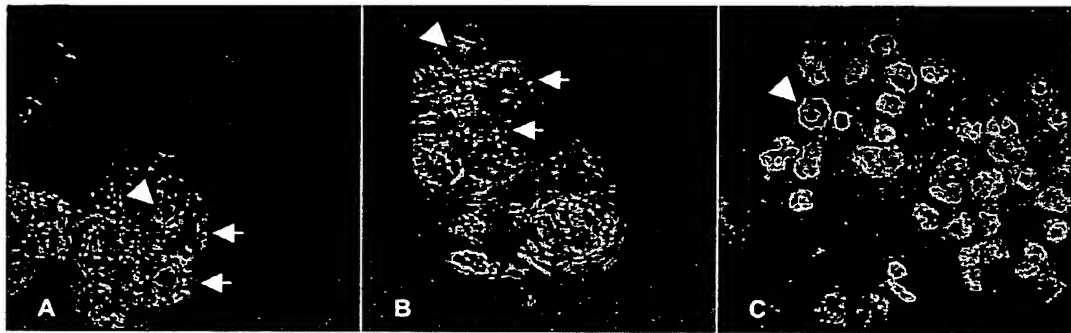


Fig. 6

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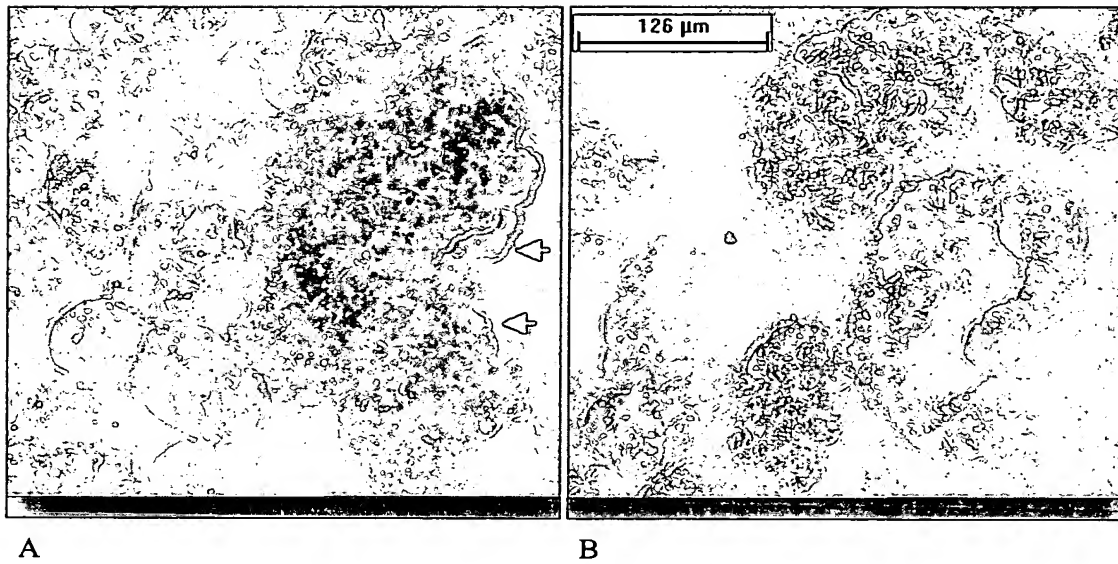


Fig. 7

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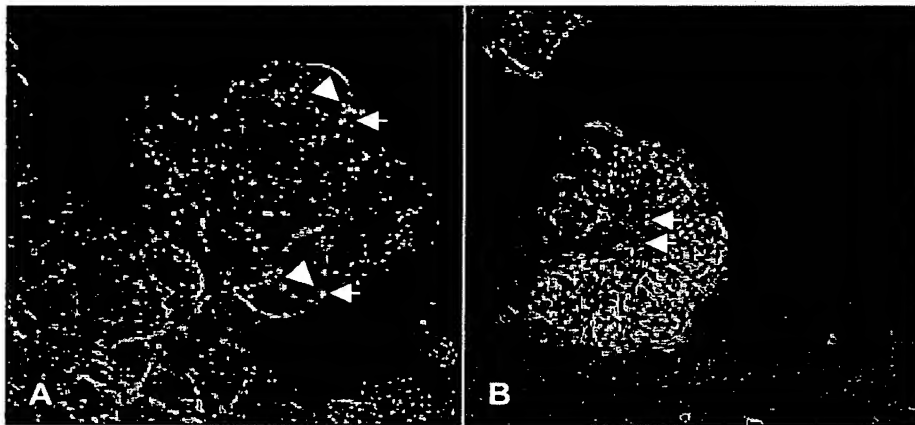


Fig. 8

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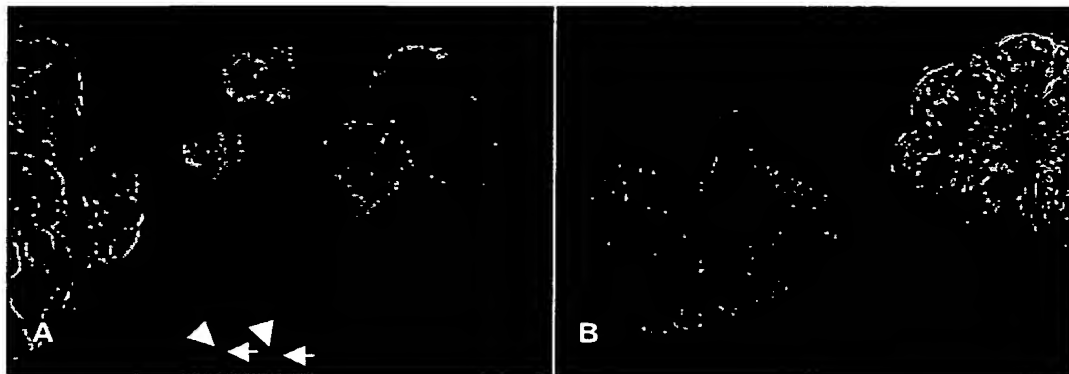




FIG. 9: VDI sequence (top) vs Sec3 Homologs (bottom)

Q9NV70 Human Exocyst complex component Sec3 (BM-012) Length = 894

5 Query: 55 LALS VKSKGPRKKAFLRMKYSSGGVLEPAKMYKLKHL SKVEVITNDPSGCTFTLGFDNL 114  
L +V ++ P + ++V K G + + L+ L+ V+ F L F+ +  
Sbjct: 38 LCATVTTERPVQVKVVKVKS DKGDFYKRQIAWALRDLAVDAKDAIKENPEFDLHFEKI 97

10 Query: 115 RSQS VAPPQWTRNTDDRNRLLVCILNICKDVLGR LPKVVGIDIVEMALWAKDNTPVVTT 174  
+W +T ++N + CI + + L + ID V N  
Sbjct: 98 Y-----KVVASSTA EKNAFISCIWKL NQRYLRK-----KIDFV-----NVSSQLL 137

15 Query: 175 QRSTEDGEPVAESVTESDLKVTVEKELVSQAEEEDMEALLGTYVMGIGEAFAF SERLKRE 234  
+ S GE +SVT D +V E + ++ EE+D+E ++ I AEAF+E+L RE  
Sbjct: 138 EESVPSGE--NQSVTGGDEEVVDEYQELNAREEQDIEIMMEGCEY AISNAEAF AEKLSRE 195

20 Query: 235 LQALEAANVHAILESEPLVDEVLNGLEAATNIVDDMDEWL GIFNIKL RHREDIESIETR 294  
LQ L+ AN+ +I+ SE V+ ++ L+ A VD ++ L + L+ ++E ++ I  
Sbjct: 196 LQVLDGANIQSIMASEKQVNILMKLLDEALKEVDQIELKLSSYEMLQSVKEQMDQISES 255

25 Query: 295 NNKLEMQSVNNKALIEELDKVIERLRVPSEYAASLTGGSFDEADMLQNI EACEWLAKALR 354  
N+ + + + NN L+ E++ ++ + + + +L G + + IEAC A AL  
Sbjct: 256 NHLIHL SNTNNVKLLSEIEFLVNHMDLAKGH IKALQEGDLASS---RGIEACTNAADALL 312

30 Query: 355 GLEVPNLDP IYANMRVKEKRAELEKLKATFVRRASEFLRNYFASLVDFM VSDKSYFSQR 414  
L P + + AVK ++ L+ F RR + L N F V S +Q  
Sbjct: 313 QCMNVALRPGHDL LLA VKQQQRFSDLR ELFARRLASHLNNVF---VQQGHDQSSTLAQH 369

35 Query: 415 G-QLKRPDHADLR YKCR TYARLLQHLKGLDKNCLGPLRKAYCSSLNLLLRREAREFAN-- 471  
+L P+H YA+L++ LK D L K Y L+ L RE ++F  
Sbjct: 370 SVELTLPNHHPFHRDLLRYAKLMEWLKSTDY GKYEGLTKNYMDYLSRLYEREIKDFF EVA 429

40 Query: 472 --ELRASTKVS-----RNPTVWLEGSTG-----SSQNANTDT 501  
++ +TK S + T L GS+G SS N + +  
Sbjct: 430 KIKMTGTTKESKKFATLPRKESAVKQETESLHGSSGKLTGSTSSLNKL SVQSSGNRRSQS 489

45 Query: 502 SAVSDA-----YAKMLTIFIPLLVDESSFFAHFMC FEVPALAPPGG 542  
S++ D + ++L+ PL + E F + F + + PG  
Sbjct: 490 SSLD MGMSASDL DVADRTKFDKIFEQVLSELEPLCLAEQDFISKFFKLQ-QHQSM PG 548

50 Query: 543 AGNDKKSQSNNDDGND DDDLGIMDIDETDKKPGKNSPDLTALNESLQD LLDGIQEDFYAV 602  
E D + + + + I+ + +  
Sbjct: 549 MAEAEDLDGGT LSRQHNCGTPLPV SSEKD-----MIRQMMIKIFRCIEPELNNL 597

55 Query: 603 VDWAYKIDPLRCISMH-GITER YLSGQKADAAGFVRLLLGDLES RVSMQFSRFVDEACHQ 661  
+ KID + M ++ + Q D A F+ LG++ V F + + Q  
Sbjct: 598 IALGDKIDSFN SLYMLVKMSHHVWTAQNVD PASFLSTTLGNVLVTVKR NFDKCISNQIRQ 657

Query: 662 IERNERNVR-QMGVLPYIPRFAALATRMEQ-YIQGQSRDLVDQAYTKFVSIMFVTLEKIA 719  
+E + + + ++G+LP++ F A E + + R +D+AYTK + +FV +EK+A  
Sbjct: 658 MEEVKISKKSKVGILPFVAEFEEFAGLAESIFKNAERRGDL DKAYTKLIRGVFVNVEKVA 717

Query: 720 QQDPKYA-DILLLENYAAFQNSLYDLANVVPTLAKFYHQASEAYEQACTRHISMIIYYQF 778  
+ K D++++EN+ +L L + L +A + Y ++ +  
Sbjct: 718 NESQKTPRDVVM MENFHHIFATLSRLK--ISCLEAEKKEAKQKYTDHLQSYVIYSLGQPL 775

## FIG. 9 Cont'd

- Query: 779 ERLFQFAKKIEDFMYT-ITPEEIPFQLGLSKVELRKMLKSSLSG-VDKSIAAMYKKLQKN 836  
 E+L F + +E + I EE+ +QL +K ELRK++K V K + +YKK+ K+  
 5 Sbjct: 776 EKLNHFFEGVEARVAQGIREEEVSQYLA FNKQELRKVIKEYPGKEVKKGLDNLKVKVDKH 835
- Query: 837 LASEE-LLPSLWDKCKKEFLDKYESFVQLVAKVYPSENV 874  
 L EE LL +W + EF+ +Y+ F L+A+ YP V  
 10 Sbjct: 836 LCEEENLLQVVWHSMQDEFIRQYKHFEGLIARCYPGSGV 874
- XP 223340.1 similar to Exocyst complex component Sec3 [Rattus norvegicus]  
 Length = 571
- 15 Query: 626 SGQKADAAGFVRLLLGDLESRVSMQFSRFVDEACHQIERNERNVR-QMGVLPYIPRFAAL 684  
 + Q D A F+ LG++ V F + + Q+E + + + ++G+LP++ F  
 Sbjct: 299 TAQNVDPASFLSTTLGNVLVTVKRNFDKCISNQIRQMEEVKISKSKVGILPFVAFEEF 358
- 20 Query: 685 ATRMEQ-YIQGQSRDLVDQAYTKFVSIMFVTLEKIAQQDPKYA-DILLENYA AFQNSLY 742  
 A E + + R +D+AYTK + +F+ +EK+A + K D++++EN+ +L  
 Sbjct: 359 AGLAESIFKSAERRGDLDAKAYTKLRGVFINVEKVANESQKTPRDVMMENFHHIFATLS 418
- 25 Query: 743 DLANVVPTLAKFYHQASEAYEQACTRHISMIIYYQFERLQFAKKIEDFMYT-ITPEEIP 801  
 L + L +A + Y ++ + E+L F + +E + I EE+  
 Sbjct: 419 RLK--ISCLEAEKKEAKQKYTDHLQSYVIYSLGQPLEKLNHFFEGVEARVAQGIREEEVS 476
- 30 Query: 802 FQLGLSKVELRKMLKSSLSG-VDKSIAAMYKKLQKNLASEE-LLPSLWDKCKKEFLDKYE 859  
 +QL +K ELRK++K V K + +YKK+ K+L EE LL +W + EF+ +Y+  
 Sbjct: 477 YQLAFNKQELRKVIKEYPGKEVKKGLDNLKVKVDKHLCEEENLLQVVWHSMQDEFIRQYK 536
- Query: 860 SFVQLVAKVYPSENV 874  
 F L+A+ YP V  
 Sbjct: 537 HFEGLIARCYPGSGV 551
- 35 Q8R3S6 SEC3 Mouse Exocyst complex component Sec3  
 AAH24678.1| Similar to Sec3-like [Mus musculus] Length = 894
- 40 Query: 55 LALSVKSKGPRKKAFLRVMKYSSGGVLEPAKMYKLKHLKSKVEVITNDPSGCTFTLGFNDL 114  
 L +V ++ P + ++V K G + + L+ L+ V+ F L F+ +  
 Sbjct: 38 LCATVTTERPVQVKVVKVKKSDKGDFYKQIAWALRDLAVVDAKDAIKENPEFDLHFEKV 97
- 45 Query: 115 RSQSVAPPQWTRNTDDRNRLVCILNICKDVLGRLPKVVGIDIVEMALWAKDNTPVVTT 174  
 +W +T ++N + CI + + L + ID V N  
 Sbjct: 98 Y-----KWASSTAENAFISCIWKLNRQLRK-----KIDFV-----NVSSQLL 137
- 50 Query: 175 QRSTEDGEPPVAESVTESDLKVTVEKELVSQAEEDMEALLGTYVMGIGEAFAFSERLKRE 234  
 + S GE +SV D + E + ++ EE+D+E ++ I AEAF+E+L RE  
 Sbjct: 138 EESVPSGE--NQSVAGGDEEAVDEYQELNAREEQDIEIMMEGCECAISNAEFAEKLSRE 195
- Query: 235 LQALEAANVHAILESEPLVDEVLNGLEAATNIVDDMDEWLGFIFNIKLHRMREDIESIETR 294  
 LQ L+ AN+ +I+ SE V+ ++ L+ A VD ++ L + L+ ++E ++ I  
 Sbjct: 196 LQVLDGANIQSIMASEKQVNTLMQLLDEALTEVDQIELKLSSYEMLQSVKEQMDQISES 255
- 55 Query: 295 NNKLEMQSVNNKALIEELDKVIERLRVPSEYAASLTGGSFDEADMLQNI EACEWLAKALR 354  
 N+ + + + NN L+ E++ ++ + + + +L G + + IEAC A AL  
 Sbjct: 256 NHLIHLSTNNVKLLSEIEFLVNHMDLAKGHKALQEGDLVSS---RGIEACTNAADALL 312

FIG. 9 Cont'd

Query: 355 GLEVPNLDPIYANMRAVKEKRAELEKLGKATFVRRASEFLRNYFASLVDFMVSCKSYFSQR 414  
 L P + + A K ++ L+ F RR + L N F V S +Q  
 5 Sbjct: 313 QCMNVALRPGHDMMLAIKQQQQRFSDLREHFARRLASHLNNVF--VQQGHDQSSTLAQH 369  
 Query: 415 G-QLKRPDHADLRYKCRTYARLLQHLKGLDKNCLGPLRKAYCSSLNLLLRREAREF 469  
 +L P+H YA+L++ LK D L K Y L+ L RE ++F  
 Sbjct: 370 SVELTLPNHHHPFHRDLLRYAKLMEWLKSTDYGYEGLTKNYMDYLSRLYEREIKDF 425

10 AAL29126.1 SD02883p [Drosophila melanogaster] Length = 889

Query: 123 QWTMRNTDDRNRLLVCILN--ICKDVLGRLPKVVGIDIVEMALWAKDNTTP-VVTTQRSTE 179  
 15 +W N +R L +LN I K V G+ + + A W + +P V R+ +  
 Sbjct: 105 KQYALNPHERQNFILA-VLNRIQKSVRGQRAEFNVV---AAWLSEKSEKVALGRAVQ 159

Query: 180 DGEFVAESVTESDLKVTVEKELVSQAEEEDMEALLGTYVMGIGEAFAFSERLKRELQALE 239  
 + + E + + E ++ E ++ L I +AE F E+L REL L+  
 20 Sbjct: 160 KTQHM--DDEEDEEEEAQEFTALTDKEANELGKLFSECDFAIKDAEQFIEQLSRELHDL 217

Query: 240 AANVHAILESEPLVDEVINGLEAATNIVDDMDEWLGIKLNHRMHREDIESIETRNKLE 299  
 AN+ ++L SE V +++ ++ A + D + L + L H++E +E I +N +E  
 25 Sbjct: 218 GANMQSVLASEQKVLKMMEHIDNAISEADKFENRLDSYEDILGHVKETMEKIGGKNAMIE 277

Query: 300 MQSVNNKALIEELDKVIERLRVPSEYAAASLTGGSFDEADMLQ-NIEACEWLAKALRGLEV 358  
 + + NN L++EL+KVI +L +P +L A+ + I A + L +A+  
 Sbjct: 278 IANNNNIKLMKELNKNVISQLDLPHSQQQALDEPDLTANGRKAIAAAQCLQQAMNS--- 334

Query: 359 PNLDPIYANMRAVKEKRAELEKLGKATFVRRASEFLRNYFASLVDFMVSCKSYFSQSGQLK 418  
 ++DP + AV++++ EK K F S F+ N F L + + D S +L  
 30 Sbjct: 335 -DIDPALLRLEAVQDQKRFEKWKQKFSATVSRFMNNLFIHLGN-EIGDMQVTST--ELT 390

Query: 419 RPDHADLRYKCRTYARLLQHLKGLDKNCLGPLRKAYCSSLNLLLRREAREFANELRAS-T 477  
 P+H+++ + Y L+ K +D+ L + Y +SL+ + R+ R F N + T  
 35 Sbjct: 391 LPNHSNVHRELTPYTELMHWTKAMDRKTYDGLMRVYTASLSKIYDRDVRNFFNLAKIQVT 450

Query: 478 KVSERNPTVWLEGSTGSSQNA-----NTDTSAVSDAYAKMLTIFI 516  
 + RN L+ ST S ++A D K+L  
 40 Sbjct: 451 EKLRNSREDLDMSTSSRKSASTIPYGTGLINRDQWGPVETADRMRFDALLEKVLAELE 510

Query: 517 PLLVDESSFFAHFMCFEVPALAPPGGAGNDKKSQSNDDGNDDDLGMIDIDETDKKPGK 576  
 P+ + E F +F +V + P D P K  
 45 Sbjct: 511 PIALQEQLFCINFFQMDVIS---PTTKNTQTTEMEKAVDMTQSIISGAVSPSGDGVPOK 567

Query: 577 NSPDLTALNESLQDLLDG---IQEDFYAVVDWAYKIDPLRCISMH-GITERYLSCQKAD 631  
 +NE ++ L+ G ++ + + + ++D + + +T+ +S Q D  
 Sbjct: 568 RID--RQINEDVRKLMMGLFGCLEPELVSIQSFERVDSFYSLYVVRILTQHVMQAQ--D 623

Query: 632 AAGFVRLLLGDLESRVSMQFSRFVDEACHQIERNERNVRQMGVLPYIPRFAALATRMEQ- 690  
 F+ + +V F RF+ I + + R +LPY+ F A E  
 50 Sbjct: 624 THSFLSMTFASALVQVKRSFDRFMQNQLLSIREAKLHKRSKAILPYVENFENFAQTAEGI 683

Query: 691 YIQGQSRDLVDQAYTKFVSIMFVLEKIAQQDPKYA-DILLLENYAAFQNSLYDLANVVP 749  
 + + R +++ Y + V+ +F ++ +Q+ PK ++ +ENY L L VP  
 55 Sbjct: 684 FRKSDRRTDMEKWYLQLVNAIFEGIQLHSQEHKPTPIQVVRMENYHMYALLAQLK--VP 741

## FIG. 9 Cont'd

Query: 750 TLAKFYHQASEAYEQACTRHISMIIYYQFERLFQFAKKIE-DFMYTITPEEIPFQLGLSK 808  
           L       +A + Y A     +++           E+L QF + ++       +   EI +Q+ SK  
 5 Sbjct: 742 GLDALKKEAKKCYNDALKAYVTQYFGRPLEKLNQFFEGVQLKVAQGVKETEISYQMAFSK 801

Query: 809 VELRKML-KSSLGVDKSIAAMYKKLQKNLASEE-LLPSLWDKCKKEFLDKYESFVQLVA 866  
           ELRK++ +       V K +   +YKK++K+L+ EE LL   +W   ++EF+ +Y   + +  
 10 Sbjct: 802 QELRKVIAQYPAREVKKGLENLYKKVEKHLSEEENLLQVVWHAMQEEFIAQYNYLEERIQ 861

Query: 867 K V Y 869  
           K Y  
 Sbjct: 862 K C Y 864

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